AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application:

LISTING OF CLAIMS:

1. - 58. (Canceled)

59. (currently amended) A method of determining polymorphic sites or sub-haplotypes for a locus that correlate with ~~a clinical response or~~an outcome of interest, comprising:

(a) providing a haplotype ~~information,~~ for each allele of the locus for each subject in a cohort of subjects and ~~clinical response or outcome data (clinical outcome values)~~an outcome value for the outcome of interest for each subject in the ~~from a~~ cohort of subjects, the locus comprising at least two polymorphic sites;

(b) statistically analyzing each individual ~~SNP~~ polymorphism in the ~~haplotype~~ haplotypes for the degree to which it correlates with the outcome of interest ~~clinical outcome values,~~ and ~~generating~~ calculating a numerical measure of the degree of correlation;

(c) saving ~~for further processing those~~ each individual ~~SNPs~~ polymorphism whose numerical measure of the degree of correlation ~~with the clinical outcome values exceeds~~ meets a first cut-off ~~value~~criterion and its numerical measure of the degree of correlation;

(d) generating all possible pair-wise combinations of the saved ~~SNPs~~ individual polymorphisms so as to provide a set of n-site sub-haplotypes where $n = 2$;

(e) statistically analyzing each newly generated n-site sub-haplotype for the degree to which it correlates with the ~~clinical outcome values~~outcome of interest and calculating ~~a~~ the numerical measure of the degree of correlation;

(f) saving ~~for further processing those~~ each n-site sub-~~haplotypes~~ haplotype whose numerical measure of the degree of correlation ~~with the clinical outcome values exceeds~~ meets the first cut-off ~~value~~criterion and its numerical measure of the degree of correlation;

(g) generating all possible pair-wise combinations among and between the saved ~~SNPs~~

individual polymorphisms and saved sub-haplotypes, to produce new ~~subhaplotypes~~ sub-haplotypes with increased values of *n*; and

(h) repeating steps (e) through (g) until either (i) no new sub-haplotypes can be generated, or (ii) no ~~further~~ new sub-haplotypes having *n* less than a pre-selected limit can be generated.

60. (currently amended) The method of claim 59, further comprising the step of displaying ~~those~~ the saved ~~SNPs~~ individual polymorphisms and sub-haplotypes whose numerical measure of the degree of correlation ~~with the clinical outcome value exceeds~~ meets a second cut-off ~~value~~criterion, wherein the second cut-off ~~value~~ criterion is ~~greater~~ more stringent than the first cut-off ~~value~~criterion.

61. (currently amended) The method of claim 59, wherein the numerical measure of the degree of correlation is ~~replaced by the~~ a p-value ~~for the correlation~~, and ~~SNPs and sub-haplotypes are saved if~~ the first cut-off criterion is that the p-value is less than or equal to a first cut-off value.

62. (currently amended) The method of claim 61, further comprising the step of displaying ~~those~~ the saved ~~SNPs~~ individual polymorphisms and sub-haplotypes whose p-value ~~for the correlation with the clinical outcome value~~ is less than or equal to a second cut-off value, wherein the second cut-off value is less than the first ~~selected~~ cut-off value.

63. (currently amended) The method of any one of claims 59-62, further comprising the step of ~~excluding from further processing~~ eliminating a complex redundant sub-haplotype ~~subhaplotypes which are constructed~~ generated from smaller saved sub-haplotypes, ~~where~~ wherein the numerical measure of the degree of correlation of each of the smaller saved sub-haplotypes ~~each have correlation values that are~~ is at least as significant as that of the complex redundant sub-haplotype.

64. (currently amended) A method of determining polymorphic sites or sub-haplotypes for a locus that correlate with ~~a clinical response or~~ an outcome of interest, comprising:

(a) providing ~~a single gene~~ haplotype for each allele of the locus for each subject in a cohort of subjects ~~information for one or more genes,~~ and ~~clinical response or outcome data, from a cohort of subjects~~an outcome value for the outcome of interest for each subject in the cohort, the locus comprising at least two polymorphic sites;

(b) statistically analyzing each ~~single gene~~ haplotype for the degree to which it correlates with the ~~clinical response or~~ outcome of interest, and calculating a numerical measure of the degree of correlation;

(c) saving ~~for further processing those haplotypes~~each haplotype whose numerical measure of the degree of correlation ~~with the clinical response or outcome of interest~~meets ~~exceeds~~ a first ~~selected value~~cut-off criterion and its numerical measure of the degree of correlation;

(d) ~~for~~ from each haplotype composed of m polymorphic sites, generating all possible sub-haplotypes having a single site masked, so as to provide a set of sub-haplotypes having $(m\text{-}n)$ sites, where $n = 1$;

(e) statistically analyzing each newly generated sub-haplotype for the degree to which it correlates with the ~~clinical response or~~ outcome of interest, and calculating ~~a~~ the numerical measure of the degree of correlation;

(f) saving ~~for further processing those~~ each sub-~~haplotypes~~ haplotype whose numerical measure of the degree of correlation ~~with the clinical response or outcome of interest exceeds~~meets the first ~~selected value~~cut-off criterion and its numerical measure of the degree of correlation;

(g) from the saved sub-haplotypes, generating all possible sub-haplotypes having one additional site masked; and

(h) repeating steps (e) through (g) until either (i) no new sub-haplotypes ~~have a degree of correlation which exceeds the first selected value,~~ or (ii) no further sub-haplotypes having more unmasked sites than a pre-selected limit can be generated.

65. (currently amended) The method of claim 64, further comprising the step of displaying those saved haplotypes and sub-haplotypes whose numerical measure of the degree of

correlation ~~with the clinical response or outcome of interest exceeds~~meets a second ~~selected value~~cut-off criterion, wherein the second ~~selected value~~cut-off criterion is ~~greater~~ more stringent than the first ~~selected value~~cut-off criterion.

66. (currently amended) The method of claim 64, wherein the numerical measure of the degree of correlation is ~~replaced by the~~a p-value ~~for the correlation,~~ and the first cut-off criterion is that ~~sub-haplotypes are saved if~~ the p-value is less than or equal to a ~~first~~-first selected value.

67. (currently amended) The method of claim 66, further comprising the step of displaying those saved haplotypes and sub-haplotypes whose p-value ~~for the correlation with the clinical response or outcome of interest~~ is less than or equal to a second selected value, wherein the second selected value is less than the first selected value.

68. (currently amended) The method of any one of claims 64-67, further comprising the step of ~~excluding from further processing~~ discarding a complex redundant sub-haplotype ~~subhaplotypes~~ which ~~are~~ is constructed from smaller saved sub-haplotypes, ~~where~~ wherein the numerical measure of the degree of correlation of each of the smaller saved sub-haplotypes ~~has correlation values that are~~ is at least as significant as that of the complex redundant sub-haplotype.

69. – 109 (canceled)

110. (currently amended) A computer-usable medium having computer-readable program code stored thereon, for causing a computer to execute a method to determine ~~polymorphic sites~~polymorphisms or sub-haplotypes for a locus that correlate with ~~a clinical response or~~ an outcome of interest, ~~or other phenotype, the computer-readable program code~~ the method comprising:

(a) ~~computer-readable program code for causing a computer to~~ accessing a database ~~containing~~ comprising a haplotype ~~information~~for each allele of the locus for each subject in a cohort of subjects, and ~~clinical response or outcome data (clinical outcome~~

~~values)~~ an outcome value for the outcome of interest for each subject in the ~~or other phenotype data, from a~~ cohort of subjects, the locus comprising at least two polymorphic sites;

(b) ~~computer-readable program code for causing a computer to~~ statistically ~~analyze~~ analyzing each individual ~~SNP~~ polymorphism in the ~~haplotype~~ haplotypes for the degree to which it correlates with the ~~clinical outcome values or other phenotype data,~~ outcome of interest and ~~generating~~ calculating a numerical measure of the degree of correlation;

(c) ~~computer-readable program code for causing a computer to store for further processing~~ storing each ~~those~~ individual ~~SNPs~~ polymorphism whose numerical measure of the degree of correlation ~~with the clinical outcome values or other phenotype data exceeds~~ meets a first cut-off ~~value~~criterion and its numerical measure of the degree of correlation;

(d) ~~computer-readable program code for causing a computer to generate~~ generating all possible pair-wise combinations of the saved ~~SNPs~~ individual polymorphisms so as to provide a set of n-site sub-haplotypes where $n = 2$;

(e) ~~computer-readable program code for causing a computer to~~ statistically ~~analyze~~ analyzing each newly generated n-site sub-haplotype for the degree to which it correlates with the ~~clinical~~ outcome of interest ~~values or other phenotype data,~~ and ~~calculate~~ calculating the a numerical measure of the degree of correlation;

(f) ~~computer-readable program code for causing a computer to store for further processing~~ storing each~~those~~ n-site sub-~~haplotypes~~ haplotype whose numerical measure of the degree of correlation ~~exceeds~~ meets the first cut-off ~~value~~criterion and its numerical measure of the degree of correlation;

(g) ~~computer-readable program code for causing a computer to generate~~ generating all possible pair-wise combinations among and between the saved ~~SNPs~~ individual polymorphisms and saved sub-haplotypes, to produce new sub-haplotypes with increased values of n; and

(h) ~~computer-readable program code for causing a computer to repeat~~ repeating steps (e) through (g) until either (i) no new sub-haplotypes can be generated, or (ii) no ~~further~~

new sub-haplotypes having *n* less than a pre-selected ~~or user-selected~~ limit can be generated.

111. (currently amended) The computer-usable medium of claim 110, wherein the method ~~which~~ further comprises ~~computer-readable program code stored thereon for causing a computer to~~ displaying ~~display~~ those saved ~~SNPs~~ individual polymorphisms and sub-haplotypes whose numerical measure of the degree of correlation ~~with the clinical outcome value or other phenotype exceeds~~meets a second cut-off ~~value~~criterion, wherein the second cut-off ~~value~~ criterion is ~~greater~~ more stringent than the first cut-off ~~value~~criterion.

112. (currently amended) A computer-usable medium having computer-readable program code stored thereon, for causing a computer to execute a method to determine polymorphic sites or sub-haplotypes for a locus that correlate with ~~a clinical response or~~ an outcome of interest, ~~or other phenotype,~~ the ~~computer-readable program code~~method comprising:

(a) ~~computer-readable program code for causing a computer to access~~ accessing a database ~~containing~~ comprising a haplotype for each allele of the locus for each subject in a cohort of subjects ~~information,~~ and an outcome value for the outcome of interest ~~clinical response or outcome data (clinical outcome values)~~ for each subject in the~~or other phenotype data, from a~~ cohort of subjects, the locus comprising at least two polymorphic sites;

(b) ~~computer-readable program code for causing a computer to~~ statistically ~~analyze~~ analyzing each individual ~~SNP~~ polymorphism in the ~~haplotype~~ haplotypes for the degree to which it correlates with the ~~clinical~~ outcome of interest ~~values or other phenotype data,~~ and ~~calculate~~ calculating the p-value for the ~~degree of~~ correlation;

(c) ~~computer-readable program code for causing a computer to store for further processing~~ storing ~~those~~ each individual ~~SNPs~~ polymorphism whose p-value ~~for the degree of correlation~~ does not exceed a first cut-off value and its p-value;

(d) ~~computer-readable program code for causing a computer to generate~~generating all possible pair-wise combinations of the saved ~~SNPs~~ individual polymorphisms so as to provide a set of *n*-site sub-haplotypes where $n = 2$;

(e) ~~computer-readable program code for causing a computer to~~ statistically ~~analyze~~ analyzing each newly generated *n*-site sub-haplotype for the degree to which it correlates with the ~~clinical~~ outcome of interest ~~values or other phenotype data,~~ and ~~calculate~~ calculating the p-value for the ~~degree of~~ correlation;

(f) ~~computer-readable program code for causing a computer to store for further processing~~ storing ~~those~~ each *n*-site sub-~~haplotypes~~ haplotype whose p-value ~~for the degree of correlation~~ does not exceed the first cut-off value and its p-value;

(g) ~~computer-readable program code for causing a computer to generate~~generating all possible pair-wise combinations among and between the saved ~~SNPs~~ individual polymorphisms and saved sub-haplotypes, to produce new subhaplotypes with increased values of *n*; and

(h) ~~computer-readable program code for causing a computer to repeat~~ repeating steps (e) through (g) until either (i) no new sub-haplotypes can be generated, or (ii) no ~~further~~ new sub-haplotypes having *n* less than a pre-selected ~~or user-selected~~ limit can be generated.

113. (currently amended) The computer-usable medium of claim 110, ~~which further comprises computer-readable program code stored thereon for causing a computer to~~ wherein the method further comprises displaying ~~display those~~ the saved ~~SNPs~~ individual polymorphisms and sub-haplotypes whose p-value ~~for the degree of correlation with the clinical outcome value or other phenotype~~ does not exceed a second cut-off value, wherein the second cut-off value is less than the first cut-off value.

114. (currently amended) The computer-usable medium of claim~~claims~~ 110-~~113~~, ~~which further comprises computer-readable program code stored thereon for causing a computer to exclude from further processing~~ wherein the method further comprises eliminating a complex redundant ~~subhaplotypes~~ subhaplotype ~~which are constructed~~generated from smaller saved sub-haplotypes, wherein the numerical measure of the degree of correlation of each of ~~where~~ the smaller saved sub-haplotypes ~~each have correlation values that are~~ is at least as significant as that of the complex redundant sub-haplotype.

115. (currently amended) A computer-usable medium having computer-readable program code stored thereon, for causing a computer to execute a method to determine polymorphic sites or sub-haplotypes for a locus that correlate with ~~a clinical response or~~ an outcome of interest~~, or other phenotype of interest~~, the ~~computer readable program code~~method comprising:

(a) ~~computer readable program code for causing a computer to access~~accessing a database ~~containing single gene~~ comprising a haplotype for each allele of the locus for each subject in a cohort of subjects ~~information for one or more genes,~~ and ~~clinical response,~~ an outcome ~~data, or other phenotype data from a~~value for the outcome of interest for each subject in the cohort of subjects, the locus comprising at least two polymorphic sites;

(b) ~~computer readable program code for causing a computer to~~ statistically ~~analyze~~ analyzing each ~~single gene~~ haplotype for the degree to which it correlates with the ~~clinical response,~~ outcome~~, or phenotype~~ of interest, and ~~to generate~~ calculating a numerical measure of the degree of correlation;

(c) ~~computer readable program code for causing a computer to store for further processing~~ storing ~~those haplotypes~~each haplotype whose numerical measure of the degree of correlation ~~exceeds~~ meets a first cut-off ~~value~~criterion and its numerical measure of the degree of correlation;

(d) ~~computer readable program code for causing a computer to generate~~generating, ~~for~~ from each haplotype composed of *m* polymorphic sites, all possible sub-haplotypes having a single site masked, so as to provide a set of *m-n* site sub-haplotypes where $n = 1$;

(e) ~~computer readable program code for causing a computer to~~ statistically ~~analyze~~ analyzing each newly generated sub-haplotype for the degree to which it correlates with the ~~clinical response,~~ outcome~~, or phenotype~~ of interest, and calculating ~~a~~ the numerical measure of the degree of correlation;

(f) ~~computer readable program code for causing a computer to save for further processing~~ storing ~~those~~ each ~~sub-haplotypes~~ haplotype whose numerical measure of the degree of correlation ~~exceeds~~ meets the first cut-off ~~value~~criterion and its numerical measure of

the degree of correlation;

(g) ~~computer-readable program code for causing a computer to generate~~generating, from the ~~saved~~ stored sub-haplotypes, all possible sub-haplotypes having one additional site masked; and

(h) ~~computer-readable program code for causing a computer to repeat~~repeating steps (e) through (g) until either (i) no new sub-haplotypes ~~have a degree of correlation which exceeds the first cut-off value~~, or (ii) no further sub-haplotypes having more unmasked sites than a pre-selected limit can be generated.

116. (currently amended) The computer-usable medium of claim 115, ~~which further comprises computer-readable program code stored thereon for causing a computer to display~~wherein the method further comprises displaying those ~~saved~~ stored haplotypes and sub-haplotypes whose numerical measure of the degree of correlation ~~with the clinical response data, outcome value, or other phenotype data exceeds~~ meets a second cut-off ~~value~~criterion, wherein the second cut-off ~~value~~ criterion is ~~greater~~ more stringent than the first cut-off ~~value~~criterion.

117. (currently amended) A computer-usable medium having computer-readable program code stored thereon, for causing a computer to execute a method to determine polymorphic sites or sub-haplotypes for a locus that correlate with ~~a clinical response or~~an outcome of interest~~, or other phenotype of interest~~, the ~~computer-readable program code~~method comprising:

(a) ~~computer-readable program code for causing a computer to access~~accessing a database ~~containing single~~ gene comprising a haplotype for each allele of the locus for each subject in a cohort of subjects ~~information for one or more genes,~~ and ~~clinical response,~~ an outcome value for the outcome of interest for each subject in the data~~, or other phenotype data from a~~ cohort of subjects, the locus comprising at least two polymorphic site;

(b) ~~computer-readable program code for causing a computer to~~ statistically ~~analyze~~ analyzing each ~~single gene~~ haplotype for the degree to which it correlates with the ~~clinical response,~~ outcome~~, or phenotype~~ of interest, and ~~to calculate~~calculating the p-

value for the ~~degree of~~ correlation;

(c) ~~computer-readable program code for causing a computer to store for further processing~~ storing ~~those each haplotypes~~ haplotype whose p-value ~~for the degree of correlation~~ does not exceed a first cut-off value and its p-value;

(d) ~~computer-readable program code for causing a computer to generate~~generating, for each haplotype composed of *m* polymorphic sites, all possible sub-haplotypes having a single site masked, so as to provide a set of *m-n* site sub-haplotypes where $n = 1$;

(e) ~~computer-readable program code for causing a computer to~~ statistically ~~analyze~~ analyzing each newly generated sub-haplotype for the degree to which it correlates with the ~~clinical response,~~ outcome~~, or phenotype~~ of interest, and calculating the p-value for the ~~degree of~~ correlation;

(f) ~~computer-readable program code for causing a computer to save for further processing~~ storing those sub-haplotypes whose p-value ~~for the degree of correlation~~ does not exceed the first cut-off value and its p-value;

(g) ~~computer-readable program code for causing a computer to generate~~generating, from the ~~saved~~ stored sub-haplotypes, all possible sub-haplotypes having one additional site masked; and

(h) ~~computer-readable program code for causing a computer to repeat~~repreating steps (e) through (g) until either (i) no new sub-haplotypes ~~have a p-value which does not the first cut-off value~~, or (ii) no further sub-haplotypes having more unmasked sites than a pre-selected limit can be generated.

118. (currently amended) The computer-usable medium of claim 117, ~~which~~ wherein the method further comprises ~~computer-readable program code stored thereon for causing a computer to display~~ displaying those ~~saved~~ stored haplotypes and sub-haplotypes whose p-value ~~for the degree of correlation with the clinical response, outcome, or phenotype of interest~~ does not exceed a second cut-off value, wherein the second cut-off value is less than the first cut-off value.

119. (currently amended) The computer-usable medium of claim 117~~claims 115-118, which~~

wherein the method further comprises ~~computer-readable program code stored thereon for causing a computer to exclude from further processing~~ discarding a complex redundant sub-~~haplotypes~~ haplotype which ~~are~~ is constructed from smaller stored sub-haplotypes, wherein the p-value of each of the smaller sub-haplotypes ~~each have correlation values that are~~ is at least as significant as that of the complex redundant sub-haplotype.

120. – 160. (canceled)

161. (currently amended) A computer programmed to execute a method to determine polymorphic sites or sub-haplotypes for a locus that correlate with ~~a clinical response or~~ an outcome of interest, ~~or other phenotype,~~ the computer comprising a memory having at least one region for storing computer executable program code and a processor for executing the program code stored in memory, wherein the ~~program code includes~~method comprises:

(a) ~~computer-readable program code for causing a computer to access~~accessing a database ~~containing~~ comprising a haplotype ~~information,~~ for each allele of the locus for each subject in a cohort of subjects and an outcome value ~~clinical response or outcome data (clinical outcome values) or other phenotype data, from a~~ for the outcome of interest for each subject in the cohort of subjects, the locus comprising at least two polymorphic sites;

(b) ~~computer-readable program code for causing a computer to~~ statistically ~~analyze~~ analyzing each individual ~~SNP~~ polymorphism in the haplotype for the degree to which it correlates with the ~~clinical~~ outcome of interest~~values or other phenotype data,~~ and ~~generating~~ calculating a numerical measure of the degree of correlation;

(c) ~~computer-readable program code for causing a computer to store for further processing~~ saving ~~those~~ each individual ~~SNPs~~ polymorphism whose numerical measure of the degree of correlation ~~with the clinical outcome values or other phenotype data~~ ~~exceeds~~meets a first cut-off ~~value~~criterion and its numerical measure of the degree of correlation;

(d) ~~computer-readable program code for causing a computer to generate~~generating all possible pair-wise combinations of the saved ~~SNPs~~ individual polymorphisms so as to provide a set of n-site sub-haplotypes where $n = 2$;

(e) ~~computer-readable program code for causing a computer to~~ statistically ~~analyze~~ analyzing each newly generated *n*-site sub-haplotype for the degree to which it correlates with the ~~clinical~~ outcome ~~values or other phenotype data,~~ of interest and ~~calculate~~ calculating ~~a~~ the numerical measure of the degree of correlation;

(f) ~~computer-readable program code for causing a computer to store for further processing~~ saving ~~those~~ each *n*-site sub-~~haplotypes~~ haplotype whose numerical measure of the degree of correlation ~~exceeds~~ meets the first cut-off ~~value~~criterion and its numerical measure of the degree of correlation;

(g) ~~computer-readable program code for causing a computer to generate~~generating all possible pair-wise combinations among and between the saved ~~SNPs~~ individual polymorphisms and saved sub-haplotypes, to produce new ~~subhaplotypes~~ sub-haplotypes with increased values of *n*; and

(h) ~~computer-readable program code for causing a computer to repeat~~repreating steps (e) through (g) until either (i) no new sub-haplotypes can be generated, or (ii) no ~~further~~ new sub-haplotypes having *n* less than a pre-selected ~~or user-selected~~ limit can be generated.

162. (currently amended) The computer of claim 161, wherein the ~~program code~~method further ~~includes~~ comprises ~~computer-readable program code for causing a computer to display~~displaying those saved ~~SNPs~~ individual polymorphisms and sub-haplotypes whose numerical measure of the degree of correlation ~~with the clinical outcome value or other phenotype exceeds~~ meets a second cut-off ~~value~~criterion, wherein the second cut-off ~~value~~ criterion is ~~greater~~ more stringent than the first cut-off ~~value~~criterion.

163. (currently amended) A computer programmed to execute a method to determine polymorphic sites or sub-haplotypes for a locus that correlate with ~~a clinical response or~~ an outcome of interest, ~~or other phenotype,~~ the computer comprising a memory having at least one region for storing computer executable program code and a processor for executing the program code stored in memory, wherein the ~~program code includes~~method comprises:

(a) ~~computer-readable program code for causing a computer to access~~accessing a database ~~containing~~ comprising a haplotype for each allele of the locus for each subject in a

cohort of subjects~~information,~~ and an outcome value for the outcome of interest for each subject in the ~~clinical response or outcome data (clinical outcome values) or other phenotype data, from a~~ cohort of subjects, the locus comprising at least two polymorphic sites;

(b) ~~computer readable program code for causing a computer to~~ statistically ~~analyze~~ analyzing each individual ~~SNP~~ polymorphism in the ~~haplotype~~ haplotypes for the degree to which it correlates with the ~~clinical~~ outcome ~~values or other phenotype data,~~ of interest and ~~calculate~~ calculating ~~the~~ a p-value for the ~~degree of~~ correlation;

(c) ~~computer readable program code for causing a computer to store for further processing~~ saving ~~those~~ each individual ~~SNPs~~ polymorphism whose p-value ~~for the degree of correlation~~ does not exceed a first cut-off value and its p-value;

(d) ~~computer readable program code for causing a computer to generate~~generating all possible pair-wise combinations of the saved ~~SNPs~~ individual polymorphisms so as to provide a set of n-site sub-haplotypes where $n = 2$;

(e) ~~computer readable program code for causing a computer to~~ statistically ~~analyze~~ analyzing each newly generated n-site sub-haplotype for the degree to which it correlates with the ~~clinical~~ outcome of interest ~~values or other phenotype data,~~ and ~~calculate~~ calculating the p-value for the ~~degree of~~ correlation;

(f) ~~computer readable program code for causing a computer to store for further processing~~ saving ~~those~~ each n-site sub-~~haplotypes~~ haplotype whose p-value ~~for the degree of correlation~~ does not exceed the first cut-off value and its p-value;

(g) ~~computer readable program code for causing a computer to generate~~generating all possible pair-wise combinations among and between the saved ~~SNPs~~ individual polymorphisms and saved sub-haplotypes, to produce new ~~subhaplotypes~~ sub-haplotypes with increased values of n; and

(h) ~~computer readable program code for causing a computer to repeat~~repeating steps (e) through (g) until either (i) no new sub-haplotypes can be generated, or (ii) no ~~further~~ new sub-haplotypes having n less than a pre-selected ~~or user selected~~ limit can be generated.

164. (currently amended) The computer of claim 161, wherein the ~~program code~~method further ~~includes~~ comprises ~~computer-readable program code for causing a computer to display~~displaying those saved ~~SNP~~individual polymorphisms and sub-haplotypes whose p-value ~~for the degree of correlation with the clinical outcome value or other phenotype~~ does not exceed a second cut-off value, wherein the second cut-off value is less than the first cut-off value.

165. (currently amended) The computer of any one of claims 161-~~164~~162, wherein the ~~program code further includes computer-readable program code for causing a computer to exclude from further processing~~ method further comprises discarding a complex redundant ~~subhaplotypes~~ sub-haplotype which ~~are constructed~~is generated from smaller saved sub-haplotypes, wherein the numerical measure of the degree of correlation of each of the smaller saved sub-haplotypes ~~each have correlation values that are~~ is at least as significant as that of the complex redundant sub-haplotype.

166. (currently amended) A computer programmed to execute a method to determine polymorphic sites or sub-haplotypes for a locus that correlate with ~~a clinical response or~~ an outcome of interest, ~~or other phenotype of interest,~~ the computer comprising a memory having at least one region for storing computer executable program code and a processor for executing the program code stored in memory, wherein the ~~program code includes~~method comprises:

(a) ~~computer-readable program code for causing a computer to access~~accessing a database ~~containing single gene~~comprising a haplotype for each allele of the locus for each subject in a cohort of subjects ~~information for one or more genes,~~ and an outcome value for the outcome of interest for each subject in the~~clinical response, outcome data, or other phenotype data from a~~ cohort of subjects, the locus comprising at least two polymorphic sites;

(b) ~~computer-readable program code for causing a computer to~~ statistically ~~analyze~~ analyzing each ~~single gene~~ haplotype for the degree to which it correlates with the ~~clinical response,~~ outcome~~, or phenotype~~ of interest, and ~~to generate~~calculating a

numerical measure of the degree of correlation;

(c) ~~computer-readable program code for causing a computer to store for further processing~~ saving ~~those~~ each ~~haplotypes~~ haplotype whose numerical measure of the degree of correlation ~~exceeds~~ meets a first cut-off ~~value~~criterion and its numerical measure of the degree of correlation;

(d) ~~computer-readable program code for causing a computer to generate~~generating, ~~for~~ from each haplotype composed of *m* polymorphic sites, all possible sub-haplotypes having a single site masked, so as to provide a set of *m-n* site sub-haplotypes where *n* = 1;

(e) ~~computer-readable program code for causing a computer to~~ statistically ~~analyze~~ analyzing each newly generated sub-haplotype for the degree to which it correlates with the ~~clinical response,~~ outcome~~, or phenotype~~ of interest, and calculating ~~a~~ the numerical measure of the degree of correlation;

(f) ~~computer-readable program code for causing a computer to save for further processing~~ saving ~~those~~ each sub-~~haplotypes~~ haplotype whose numerical measure of the degree of correlation ~~exceeds~~ meets the first cut-off ~~value~~criterion and its numerical measure of the degree of correlation;

(g) ~~computer-readable program code for causing a computer to generate~~generating, from the saved sub-haplotypes, all possible sub-haplotypes having one additional site masked; and

(h) ~~computer-readable program code for causing a computer to repeat~~ repeating steps (e) through (g) until either (i) no new sub-haplotypes ~~have a degree of correlation which exceeds the first cut-off value~~, or (ii) no further sub-haplotypes having more unmasked sites than a pre-selected limit can be generated.

167. (currently amended) The computer of claim 166, wherein the ~~program code~~method further ~~includes~~ comprises ~~computer-readable program code for causing a computer to display~~displaying those saved haplotypes and sub-haplotypes whose numerical measure of the degree of correlation ~~with the clinical response data, outcome value, or other phenotype data exceeds~~meets a second cut-off ~~value~~criterion, wherein the second cut-off ~~value~~

criterion is ~~greater~~ more stringent than the first cut-off ~~value~~criterion.

168. (currently amended) A computer programmed to execute a method to determine polymorphic sites or sub-haplotypes for a locus that correlate with ~~a clinical response or~~ an outcome of interest, ~~or other phenotype of interest,~~ the computer comprising a memory having at least one region for storing computer executable program code and a processor for executing the program code stored in memory, wherein the ~~program code includes~~method comprises:

(a) ~~computer readable program code for causing a computer to access~~ accessing a database ~~containing single gene~~comprising a haplotype for each allele of the locus for each subject in a cohort of subjects~~information for one or more genes,~~ and ~~clinical response,~~an outcome ~~data, or other phenotype data from a~~ value for the outcome of interest for each subject in the cohort of subjects, the locus comprising at least two polymorphic sites;

(b) ~~computer readable program code for causing a computer to~~ statistically ~~analyze~~ analyzing each ~~single gene~~ haplotype for the degree to which it correlates with the ~~clinical response,~~ outcome~~, or phenotype~~ of interest, and ~~to calculate~~calculating ~~the~~ a p-value for the ~~degree of~~ correlation;

(c) ~~computer readable program code for causing a computer to store for further processing~~ saving ~~those~~ each haplotype ~~haplotypes~~ whose p-value ~~for the degree of correlation~~ does not exceed a first cut-off value and its p-value;

(d) ~~computer readable program code for causing a computer to generate~~generating, ~~for~~ from each haplotype composed of *m* polymorphic sites, all possible sub-haplotypes having a single site masked, so as to provide a set of *m-n* site sub-haplotypes where *n* = 1;

(e) ~~computer readable program code for causing a computer to~~ statistically ~~analyze~~ analyzing each newly generated sub-haplotype for the degree to which it correlates with the ~~clinical response,~~ outcome~~, or phenotype~~ of interest, and calculating the p-value for the ~~degree of~~ correlation;

(f) ~~computer readable program code for causing a computer to save for further processing~~

saving ~~those~~ each sub-~~haplotypes~~ haplotype whose p-value ~~for the degree of correlation~~ does not exceed the first cut-off value and its p-value;

(g) ~~computer-readable program code for causing a computer to generate~~generating, from the saved sub-haplotypes, all possible sub-haplotypes having one additional site masked; and

(h) ~~computer-readable program code for causing a computer to repeat~~repeating steps (e) through (g) until either (i) no new sub-haplotypes ~~have a p-value which does not the first cut-off value,~~ or (ii) no further sub-haplotypes having more unmasked sites than a pre-selected limit can be generated.

169. (currently amended) The computer of claim 168, wherein the ~~program code~~method further ~~includes~~ comprises ~~computer-readable program code for causing a computer to display~~displaying those saved haplotypes and sub-haplotypes whose p-value ~~for the degree of correlation with the clinical response, outcome, or phenotype of interest~~ does not exceed a second cut-off value, wherein the second cut-off value is less than the first cut-off value.

170. (currently amended) The computer of any one of claims 166-~~169~~167, wherein the ~~program code~~method further ~~includes computer-readable program code for causing a computer to exclude from further processing~~comprises discarding a complex redundant sub-~~haplotypes~~ haplotype which ~~are~~ is constructed from smaller saved sub-haplotypes, ~~where~~ wherein the numerical measure of the degree of correlation of each of the smaller saved sub-haplotypes ~~each have correlation values that are~~ is at least as significant as that of the complex redundant sub-haplotype.

171. – 183. (canceled)

184. (new) The method of claim 59, wherein providing comprises determining the haplotype for each allele of the locus for each subject and acquiring the outcome value for the outcome of interest for each subject.

185. (new) The method of claim 60, further comprising displaying the numerical measure of the degree of correlation of each displayed individual polymorphism or sub-haplotype.

186. (new) The method of claim 64, wherein providing comprises determining the haplotype for each allele of the locus for each subject and acquiring the outcome value for the outcome of interest for each subject.

187. (new) The method of claim 65, further comprising displaying the numerical measure of the degree of correlation of each displayed haplotype or sub-haplotype.

188. (new) A method of determining polymorphic sites or sub-haplotypes for a locus that correlate with an outcome of interest, comprising:

(a) providing a haplotype for each allele of the locus for each subject in a cohort of subjects and an outcome value for the outcome of interest for each subject in the cohort of subjects, the locus comprising at least two polymorphic sites;

(b) statistically analyzing each individual polymorphism in the haplotypes for the degree to which it correlates with the outcome of interest and calculating a numerical measure of the degree of correlation;

(c) saving each individual polymorphism whose numerical measure of the degree of correlation meets a first cut-off criterion for statistical significance;

(d) generating all possible pair-wise combinations of the saved individual polymorphisms so as to provide a set of n-site sub-haplotypes where $n = 2$;

(e) statistically analyzing each newly generated n-site sub-haplotype for the degree to which it correlates with the outcome of interest and calculating the numerical measure of the degree of correlation;

(f) saving each n-site sub-haplotype whose numerical measure of the degree of correlation meets the first cut-off criterion;

(g) generating all possible pair-wise combinations among and between the saved individual polymorphisms and saved sub-haplotypes, to produce new sub-haplotypes with increased values of n; and

(h) repeating steps (e) through (g) until either (i) no new sub-haplotypes or (ii) no new sub-

haplotypes having *n* less than a pre-selected limit can be generated.

189. (new) The method of claim 188, wherein providing comprises determining the haplotype for each allele of the locus for each subject and acquiring the outcome value for the outcome of interest for each subject.

190. (new) The method of claim 188, further comprising saving the numerical measure of the degree of correlation of each saved individual polymorphism or sub-haplotype.